

indicated (consensus; SEQ ID NO:9). Bold, underlined residues represent the preferred peptides.

Replace the paragraph beginning at page 4, line 13, with the following rewritten paragraph:

Fig. 5, the common motif within peptides 6 (amino acid residues 31 to 46 of SEQ ID NO:6), 7 (amino acid residues 37 to 52 of SEQ ID NO:6) and R5 (amino acid residues 61 to 80 of SEQ ID NO:7), V--E--WG-P (amino acid residues 18 to 22 of SEQ ID NO:9) is shown.

Replace the paragraph beginning at page 12, line 9, with the following rewritten paragraph:

It is interesting to note that one of the two self protective epitopes is the self peptide 5, which is the homologous rat epitope to the bacterial protective peptide 6. Moreover, immunization with the bacterial peptides 6 and 7 and with the mammalian peptide 5 led to the production of anti bacterial HSP 6 and anti bacterial HSP antibodies, as well as protection against disease induction. Observing the primary structure of these three peptides leads to the conclusion that they express a common motif (V--E--W G-P; amino acid residues 18 to 22 of SEQ ID NO:9) which might be the protective motif of these peptides (Figure. 5).

Replace Table 4 beginning at page 20, line 1, with the following rewritten table:

Table 4
Potential epitopes of MT HSP 65kD

Location of the peptide (aa residues of SEQ ID NO:6)	Sequence of the peptide	Length	Experimental peptide matching
35-43	<u>G-RNVVLEKKW-G</u>	9	6,7
123-132	<u>A-VEKVTETLLK-G</u>	10	21
135-143	<u>A-KEVETKEQI-A</u>	9	21
319-332	RKVVVTKDAETTIVE	14	none
357-367	<u>S-DYDREKLQERL-A</u>	11	59
383-396	<u>A-TEVELKERKHRIED-A</u>	14	63
183-195	<u>G-LQLELTEGMRFDK-G</u>	13	31
259-270	S-TLVVN <u>KIRGTFK-S</u>	12	45